

RAW SEQUENCE LISTING

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Application Serial Number: 10/577,008
Source: 1/FWD
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/577,008

DATE: 01/19/2007

TIME: 16:40:54

Input Set : A:\2007-01-11 3749-0112PUS1.txt
 Output Set: N:\CRF4\01192007\J577008.raw

3 <110> APPLICANT: SUZUKI, Toshiharu et al.
 5 <120> TITLE OF INVENTION: MARKER PEPTIDE FOR ALZHEIMER'S DISEASE
 7 <130> FILE REFERENCE: 3749-0112PUS1
 9 <140> CURRENT APPLICATION NUMBER: US 10/577,008
 10 <141> CURRENT FILING DATE: 2006-04-25
 12 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/016209
 13 <151> PRIOR FILING DATE: 2004-11-01
 15 <150> PRIOR APPLICATION NUMBER: JP 2003/375363
 16 <151> PRIOR FILING DATE: 2003-11-05
 18 <160> NUMBER OF SEQ ID NOS: 13
 20 <170> SOFTWARE: PatentIn Ver. 2.0
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 971
 24 <212> TYPE: PRT
 25 <213> ORGANISM: human
 27 <400> SEQUENCE: 1
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 29 1 5 10. 15
 31 Leu Ala Gly Leu Leu Cys Gly Gly Gly Val Trp Ala Ala Arg Val Asn
 32 20 25 30
 34 Lys His Lys Pro Trp Leu Glu Pro Thr Tyr His Gly Ile Val Thr Glu
 35 35 40 45
 37 Asn Asp Asn Thr Val Leu Leu Asp Pro Pro Leu Ile Ala Leu Asp Lys
 38 50 55 60
 40 Asp Ala Pro Leu Arg Phe Ala Gly Glu Ile Cys Gly Phe Lys Ile His
 41 65 70 75 80
 43 Gly Gln Asn Val Pro Phe Asp Ala Val Val Val Asp Lys Ser Thr Gly
 44 85 90 95
 46 Glu Gly Val Ile Arg Ser Lys Glu Lys Leu Asp Cys Glu Leu Gln Lys
 47 100 105 110
 49 Asp Tyr Ser Phe Thr Ile Gln Ala Tyr Asp Cys Gly Lys Gly Pro Asp
 50 115 120 125
 52 Gly Thr Asn Val Lys Lys Ser His Lys Ala Thr Val His Ile Gln Val
 53 130 135 140
 55 Asn Asp Val Asn Glu Tyr Ala Pro Val Phe Lys Glu Lys Ser Tyr Lys
 56 145 150 155 160
 58 Ala Thr Val Ile Glu Gly Lys Gln Tyr Asp Ser Ile Leu Arg Val Glu
 59 165 170 175
 61 Ala Val Asp Ala Asp Cys Ser Pro Gln Phe Ser Gln Ile Cys Ser Tyr
 62 180 185 190
 64 Glu Ile Ile Thr Pro Asp Val Pro Phe Thr Val Asp Lys Asp Gly Tyr
 65 195 200 205
 67 Ile Lys Asn Thr Glu Lys Leu Asn Tyr Gly Lys Glu His Gln Tyr Lys

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68	210	215	220
70	Leu Thr Val Thr Ala Tyr Asp Cys Gly Lys Lys Arg Ala Thr Glu Asp		
71	225	230	235
			240
73	Val Leu Val Lys Ile Ser Ile Lys Pro Thr Cys Thr Pro Gly Trp Gln		
74	245	250	255
76	Gly Trp Asn Asn Arg Ile Glu Tyr Glu Pro Gly Thr Gly Ala Leu Ala		
77	260	265	270
79	Val Phe Pro Asn Ile His Leu Glu Thr Cys Asp Glu Pro Val Ala Ser		
80	275	280	285
82	Val Gln Ala Thr Val Glu Leu Glu Thr Ser His Ile Gly Lys Gly Cys		
83	290	295	300
85	Asp Arg Asp Thr Tyr Ser Glu Lys Ser Leu His Arg Leu Cys Gly Ala		
86	305	310	315
			320
88	Ala Ala Gly Thr Ala Glu Leu Leu Pro Ser Pro Ser Gly Ser Leu Asn		
89	325	330	335
91	Trp Thr Met Gly Leu Pro Thr Asp Asn Gly His Asp Ser Asp Gln Val		
92	340	345	350
94	Phe Glu Phe Asn Gly Thr Gln Ala Val Arg Ile Pro Asp Gly Val Val		
95	355	360	365
97	Ser Val Ser Pro Lys Glu Pro Phe Thr Ile Ser Val Trp Met Arg His		
98	370	375	380
100	Gly Pro Phe Gly Arg Lys Lys Glu Thr Ile Leu Cys Ser Ser Asp Lys		
101	385	390	395
			400
103	Thr Asp Met Asn Arg His His Tyr Ser Leu Tyr Val His Gly Cys Arg		
104	405	410	415
106	Leu Ile Phe Leu Phe Arg Gln Asp Pro Ser Glu Glu Lys Lys Tyr Arg		
107	420	425	430
109	Pro Ala Glu Phe His Trp Lys Leu Asn Gln Val Cys Asp Glu Glu Trp		
110	435	440	445
112	His His Tyr Val Leu Asn Val Glu Phe Pro Ser Val Thr Leu Tyr Val		
113	450	455	460
115	Asp Gly Thr Ser His Glu Pro Phe Ser Val Thr Glu Asp Tyr Pro Leu		
116	465	470	475
			480
118	His Pro Ser Lys Ile Glu Thr Gln Leu Val Val Gly Ala Cys Trp Gln		
119	485	490	495
121	Glu Phe Ser Gly Val Glu Asn Asp Asn Glu Thr Glu Pro Val Thr Val		
122	500	505	510
124	Ala Ser Ala Gly Gly Asp Leu His Met Thr Gln Phe Phe Arg Gly Asn		
125	515	520	525
127	Leu Ala Gly Leu Thr Leu Arg Ser Gly Lys Leu Ala Asp Lys Lys Val		
128	530	535	540
130	Ile Asp Cys Leu Tyr Thr Cys Lys Glu Gly Leu Asp Leu Gln Val Leu		
131	545	550	555
			560
133	Glu Asp Ser Gly Arg Gly Val Gln Ile Gln Ala His Pro Ser Gln Leu		
134	565	570	575
136	Val Leu Thr Leu Glu Gly Glu Asp Leu Gly Glu Leu Asp Lys Ala Met		
137	580	585	590
139	Gln His Ile Ser Tyr Leu Asn Ser Arg Gln Phe Pro Thr Pro Gly Ile		
140	595	600	605

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142 Arg Arg Leu Lys Ile Thr Ser Thr Ile Lys Cys Phe Asn Glu Ala Thr
143 610 615 620
145 Cys Ile Ser Val Pro Pro Val Asp Gly Tyr Val Met Val Leu Gln Pro
146 625 630 635 640
148 Glu Glu Pro Lys Ile Ser Leu Ser Gly Val His His Phe Ala Arg Ala
149 645 650 655
151 Ala Ser Glu Phe Glu Ser Ser Glu Gly Val Phe Leu Phe Pro Glu Leu
152 660 665 670
154 Arg Ile Ile Ser Thr Ile Thr Arg Glu Val Glu Pro Glu Gly Asp Gly
155 675 680 685
157 Ala Glu Asp Pro Thr Val Gln Glu Ser Leu Val Ser Glu Glu Ile Val
158 690 695 700
160 His Asp Leu Asp Thr Cys Glu Val Thr Val Glu Gly Glu Glu Leu Asn
161 705 710 715 720
163 His Glu Gln Glu Ser Leu Glu Val Asp Met Ala Arg Leu Gln Gln Lys
164 725 730 735
166 Gly Ile Glu Val Ser Ser Ser Glu Leu Gly Met Thr Phe Thr Gly Val
167 740 745 750
169 Asp Thr Met Ala Ser Tyr Glu Glu Val Leu His Leu Leu Arg Tyr Arg
170 755 760 765
172 Asn Trp His Ala Arg Ser Leu Leu Asp Arg Lys Phe Lys Leu Ile Cys
173 770 775 780
175 Ser Glu Leu Asn Gly Arg Tyr Ile Ser Asn Glu Phe Lys Val Glu Val
176 785 790 795 800
178 Asn Val Ile His Thr Ala Asn Pro Met Glu His Ala Asn His Met Ala
179 805 810 815
181 Ala Gln Pro Gln Phe Val His Pro Glu His Arg Ser Phe Val Asp Leu
182 820 825 830
184 Ser Gly His Asn Leu Ala Asn Pro His Pro Phe Ala Val Val Pro Ser
185 835 840 845
187 Thr Ala Thr Val Val Ile Val Val Cys Val Ser Phe Leu Val Phe Met
188 850 855 860
190 Ile Ile Leu Gly Val Phe Arg Ile Arg Ala Ala His Arg Arg Thr Met
191 865 870 875 880
193 Arg Asp Gln Asp Thr Gly Lys Glu Asn Glu Met Asp Trp Asp Asp Ser
194 885 890 895
196 Ala Leu Thr Ile Thr Val Asn Pro Met Glu Thr Tyr Glu Asp Gln His
197 900 905 910
199 Ser Ser Glu Glu Glu Glu Glu Glu Glu Glu Ser Glu Asp
200 915 920 925
202 Gly Glu Glu Glu Asp Asp Ile Thr Ser Ala Glu Ser Glu Ser Ser Glu
203 930 935 940
205 Glu Glu Glu Gly Glu Gln Gly Asp Pro Gln Asn Ala Thr Arg Gln Gln
206 945 950 955 960
208 Gln Leu Glu Trp Asp Asp Ser Thr Leu Ser Tyr
209 965 970
211 <210> SEQ ID NO: 2
212 <211> LENGTH: 968
213 <212> TYPE: PRT

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214 <213> ORGANISM: human
216 <400> SEQUENCE: 2
217 Met Val Leu Gly Cys Glu Leu Ser Gly Ser Thr Arg Val Val Val Gly
218 1 5 10 15
220 Val Glu Ala Leu Leu Thr Gly Ala Ser Ser Pro Leu Pro Gly Val Gly
221 20 25 30
223 Pro Ala Asn Lys His Lys Pro Trp Ile Glu Ala Glu Tyr Gln Gly Ile
224 35 40 45
226 Val Met Glu Asn Asp Asn Thr Val Leu Leu Asn Pro Pro Leu Phe Ala
227 50 55 60
229 Leu Asp Lys Asp Ala Pro Leu Arg Tyr Ala Gly Glu Ile Cys Gly Phe
230 65 70 75 80
232 Arg Leu His Gly Ser Gly Val Pro Phe Glu Ala Val Ile Leu Asp Lys
233 85 90 95
235 Ala Thr Gly Glu Gly Leu Ile Arg Ala Lys Glu Pro Val Asp Cys Glu
236 100 105 110
238 Ala Gln Lys Glu His Thr Phe Thr Ile Gln Ala Tyr Asp Cys Gly Glu
239 115 120 125
241 Gly Pro Asp Gly Ala Asn Thr Lys Lys Ser His Lys Ala Thr Val His
242 130 135 140
244 Val Arg Val Asn Asp Val Asn Glu Phe Ala Pro Val Phe Val Glu Arg
245 145 150 155 160
247 Leu Tyr Arg Ala Ala Val Thr Glu Gly Lys Leu Tyr Asp Arg Ile Leu
248 165 170 175
250 Arg Val Glu Ala Ile Asp Gly Asp Cys Ser Pro Gln Tyr Ser Gln Ile
251 180 185 190
253 Cys Tyr Tyr Glu Ile Leu Thr Pro Asn Thr Pro Phe Leu Ile Asp Asn
254 195 200 205
256 Asp Gly Asn Ile Glu Asn Thr Glu Lys Leu Gln Tyr Ser Gly Glu Arg
257 210 215 220
259 Leu Tyr Lys Phe Thr Val Thr Ala Tyr Asp Cys Gly Lys Lys Arg Ala
260 225 230 235 240
262 Ala Asp Asp Ala Glu Val Glu Ile Gln Val Lys Pro Thr Cys Lys Pro
263 245 250 255
265 Ser Trp Gln Gly Trp Asn Lys Arg Ile Glu Tyr Ala Pro Gly Ala Gly
266 260 265 270
268 Ser Leu Ala Leu Phe Pro Gly Ile Arg Leu Glu Thr Cys Asp Glu Pro
269 275 280 285
271 Leu Trp Asn Ile Gln Ala Thr Ile Glu Leu Gln Thr Ser His Val Ala
272 290 295 300
274 Lys Gly Cys Asp Arg Asp Asn Tyr Ser Glu Arg Ala Leu Arg Lys Leu
275 305 310 315 320
277 Cys Gly Ala Ala Thr Gly Glu Val Asp Leu Leu Pro Met Pro Gly Pro
278 325 330 335
280 Asn Ala Asn Trp Thr Ala Gly Leu Ser Val His Tyr Ser Gln Asp Ser
281 340 345 350
283 Ser Leu Ile Tyr Trp Phe Asn Gly Thr Gln Ala Val Gln Val Pro Leu
284 355 360 365
286 Gly Gly Pro Ser Gly Leu Gly Ser Gly Pro Gln Asp Ser Leu Ser Asp

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287	370	375	380
289	His Phe Thr Leu Ser Phe Trp Met Lys His Gly Val Thr Pro Asn Lys		
290	385	390	395
292	Gly Lys Lys Glu Glu Glu Thr Ile Val Cys Asn Thr Val Gln Asn Glu		400
293	405	410	415
295	Asp Gly Phe Ser His Tyr Ser Leu Thr Val His Gly Cys Arg Ile Ala		
296	420	425	430
298	Phe Leu Tyr Trp Pro Leu Leu Glu Ser Ala Arg Pro Val Lys Phe Leu		
299	435	440	445
301	Trp Lys Leu Glu Gln Val Cys Asp Asp Glu Trp His His Tyr Ala Leu		
302	450	455	460
304	Asn Leu Glu Phe Pro Thr Val Thr Leu Tyr Thr Asp Gly Ile Ser Phe		
305	465	470	475
307	480	485	490
308	Asp Pro Ala Leu Ile His Asp Asn Gly Leu Ile His Pro Pro Arg Arg		495
310	500	505	510
313	Glu Pro Ala Leu Met Ile Gly Ala Cys Trp Thr Glu Glu Lys Asn Lys		
314	515	520	525
316	Leu Ser Ile His His Tyr Phe His Gly Tyr Leu Ala Gly Phe Ser Val		
317	530	535	540
319	Arg Ser Gly Arg Leu Glu Ser Arg Glu Val Ile Glu Cys Leu Tyr Ala		
320	545	550	555
322	Cys Arg Glu Gly Leu Asp Tyr Arg Asp Phe Glu Ser Leu Gly Lys Gly		560
323	565	570	575
325	Met Lys Val His Val Asn Pro Ser Gln Ser Leu Leu Thr Leu Glu Gly		
326	580	585	590
328	Asp Asp Val Glu Thr Phe Asn His Ala Leu Gln His Val Ala Tyr Met		
329	595	600	605
331	Asn Thr Leu Arg Phe Ala Thr Pro Gly Val Arg Pro Leu Arg Leu Thr		
332	610	615	620
334	Thr Ala Val Lys Cys Phe Ser Glu Glu Ser Cys Val Ser Ile Pro Glu		
335	625	630	635
337	640	645	650
338	Val Glu Gly Tyr Val Val Val Leu Gln Pro Asp Ala Pro Gln Ile Leu		655
340	660	665	670
341	Leu Ser Gly Thr Ala His Phe Ala Arg Pro Ala Val Asp Phe Glu Gly		
343	675	680	685
346	Asn Gly Val Pro Leu Phe Pro Asp Leu Gln Ile Thr Cys Ser Ile		
347	690	695	700
349	Ser His Gln Val Glu Ala Lys Lys Asp Glu Ser Trp Gln Gly Thr Val		
350	705	710	715
352	720	725	730
353	Glu Ile Ser Leu Val Gly Asp Asp Leu Asp Pro Glu Arg Glu Ser Leu		735
355	740	745	750
356	Leu Leu Asp Thr Thr Ser Leu Gln Gln Arg Gly Leu Glu Leu Thr Asn		
358	750	755	760
359	Thr Ser Ala Tyr Leu Thr Ile Ala Gly Val Glu Ser Ile Thr Val Tyr		765

VERIFICATION SUMMARY

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